311

#2

RAW SEQUENCE LISTING   DATE: 02/22/2002
PATENT APPLICATION: US/10/061,727   TIME: 16:08:42

Input Set : A:\3151-A SeqListce 102601.txt
Output Set: N:\CRF3\02222002\J061727.raw

```
  3 <110> APPLICANT: Sims, John E.
  4        Smith, Dirk E.
  6 <120> TITLE OF INVENTION: IL-1 RECEPTOR ACCESSORY PROTEIN
  8 <130> FILE REFERENCE: 3151-A
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/061,727
 11 <141> CURRENT FILING DATE: 2001-10-26
 13 <150> PRIOR APPLICATION NUMBER: US 60/244,831
 14 <151> PRIOR FILING DATE: 2000-10-31
 16 <160> NUMBER OF SEQ ID NOS: 4
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2064
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(2064)
 28 <223> OTHER INFORMATION:
 31 <220> FEATURE:
 32 <221> NAME/KEY: misc_feature
 33 <222> LOCATION: (1792)..(1792)
 34 <223> OTHER INFORMATION: "n" = a or c. Xaa at amino acid position 598 is Thr or Pro.
 37 <400> SEQUENCE: 1
 38 atg aca ctt ctg tgg tgt gta gtg agt ctc tac ttt tat gga atc ctg      48
 39 Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
 40 1               5                   10                  15
 42 caa agt gat gcc tca gaa cgc tgc gat gac tgg gga cta gac acc atg      96
 43 Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
 44             20                  25                  30
 46 agg caa atc caa gtg ttt gaa gat gag cca gct cgc atc aag tgc cca     144
 47 Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
 48         35                  40                  45
 50 ctc ttt gaa cac ttc ttg aaa ttc aac tac agc aca gcc cat tca gct     192
 51 Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
 52     50                  55                  60
 54 ggc ctt act ctg atc tgg tat tgg act agg cag gac cgg gac ctt gag     240
 55 Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
 56 65                  70                  75                  80
 58 gag cca att aac ttc cgc ctc ccc gag aac cgc att agt aag gag aaa     288
 59 Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
 60                 85                  90                  95
 62 gat gtg ctg tgg ttc cgg ccc act ctc ctc aat gac act ggc aac tat     336
 63 Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
```

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Input Set : A:\3151-A SeqListce 102601.txt
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64              100                 105                 110
66 acc tgc atg tta agg aac act aca tat tgc agc aaa gtt gca ttt ccc        384
67 Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
68              115                 120                 125
70 ttg gaa gtt gtt caa aaa gac agc tgt ttc aat tcc ccc atg aaa ctc        432
71 Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
72              130                 135                 140
74 cca gtg cat aaa ctg tat ata gaa tat ggc att cag agg atc act tgt        480
75 Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
76 145             150                 155                 160
78 cca aat gta gat gga tat ttt cct tcc agt gtc aaa ccg act atc act        528
79 Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
80              165                 170                 175
82 tgg tat atg ggc tgt tat aaa ata cag aat ttt aat aat gta ata ccc        576
83 Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
84              180                 185                 190
86 gaa ggt atg aac ttg agt ttc ctc att gcc tta att tca aat aat gga        624
87 Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
88              195                 200                 205
90 aat tac aca tgt gtt gtt aca tat cca gaa aat gga cgt acg ttt cat        672
91 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
92              210                 215                 220
94 ctc acc agg act ctg act gta aag gta gta ggc tct cca aaa aat gca        720
95 Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
96 225             230                 235                 240
98 gtg ccc cct gtg atc cat tca cct aat gat cat gtg gtc tat gag aaa        768
99 Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
100             245                 250                 255
102 gaa cca gga gag gag cta ctc att ccc tgt acg gtc tat ttt agt ttt       816
103 Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
104             260                 265                 270
106 ctg atg gat tct cgc aat gag gtt tgg tgg acc att gat gga aaa aaa       864
107 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
108             275                 280                 285
110 cct gat gac atc act att gat gtc acc att aac gaa agt ata agt cat       912
111 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
112             290                 295                 300
114 agt aga aca gaa gat gaa aca aga act cag att ttg agc atc aag aaa       960
115 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
116 305             310                 315                 320
118 gtt acc tct gag gat ctc aag cgc agc tat gtc tgt cat gct aga agt       1008
119 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
120             325                 330                 335
122 gcc aaa ggc gaa gtt gcc aaa gca gcc aag gtg aag cag aaa gtg cca       1056
123 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
124             340                 345                 350
126 gct cca aga tac aca gtg gaa ctg gct tgt ggt ttt gga gcc aca gtc       1104
127 Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
128             355                 360                 365
```

```
     130 ctg cta gtg gtg att ctc att gtt gtt tac cat gtt tac tgg cta gag     1152
     131 Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
     132     370             375             380
     134 atg gtc cta ttt tac cgg gct cat ttt gga aca gat gaa acc att tta     1200
     135 Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
     136 385             390             395             400
     138 gat gga aaa gag tat gat att tat gta tcc tat gca agg aat gcg gaa     1248
     139 Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
     140             405             410             415
     142 gaa gaa gaa ttt gta tta ctg acc ctc cgt gga gtt ttg gag aat gaa     1296
     143 Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
     144             420             425             430
     146 ttt gga tac aag ctg tgc atc ttt gac cga gac agt ctg cct ggg gga     1344
     147 Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
     148             435             440             445
     150 aat aca gtg gaa gca gtt ttt gat ttc att cag aga agc aga agg atg     1392
     151 Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
     152     450             455             460
     154 att gtt gtt ctg agc cct gac tat gtg aca gaa aag agc atc agc atg     1440
     155 Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
     156 465             470             475             480
     158 ctg gag ttt aaa ctg ggt gtc atg tgc cag aac tcc att gcc acc aag     1488
     159 Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
     160             485             490             495
     162 ctc att gtg gtt gag tac cgt ccc ctt gag cac ccg cac cca ggc att     1536
     163 Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
     164             500             505             510
     166 ctt cag ctc aaa gag tct gtg tct ttt gtg agc tgg aag gga gaa aag     1584
     167 Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
     168     515             520             525
     170 tcc aaa cat tct ggc tct aaa ttc tgg aaa gct ttg cgg ttg gct ctt     1632
     171 Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
     172     530             535             540
     174 ccc ctg aga agt ctg agt gcc agt tct ggc tgg aat gag agc tgc tct     1680
     175 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
     176 545             550             555             560
     178 tcc cag tct gac atc agt ctg gat cac gtt caa agg agg aga agt cgt     1728
     179 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
     180             565             570             575
     182 ttg aaa gag ccc cca gaa ctt cag agc tca gag agg gct gca ggt agc     1776
     183 Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
     184             580             585             590
W--> 186 cct cca gcc cca ggc nca atg tcc aag cac cga ggg aag tcc tcc gcc     1824
W--> 187 Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
     188             595             600             605
     190 acc tgc cgc tgt tgt gtc acc tac tgt gaa gga gag aat cac ctt agg     1872
     191 Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
     192     610             615             620
     194 aac aag agc cgg gca gag att cat aac cag ccc cag tgg gag aca cac     1920
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PATENT APPLICATION: US/10/061,727   TIME: 16:08:42

Input Set : A:\3151-A SeqListce 102601.txt
Output Set: N:\CRF3\02222002\J061727.raw

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195 Asn Lys Ser Arg Ala Glu Ile His Asn Gln Pro Gln Trp Glu Thr His
196 625             630             635             640
198 ctc tgt aag cct gtt ccc caa gag tca gaa act caa tgg ata caa aat   1968
199 Leu Cys Lys Pro Val Pro Gln Glu Ser Glu Thr Gln Trp Ile Gln Asn
200           645             650             655
202 ggc acc aga ttg gaa ccc cct gct ccc cag atc tca gcc ctt gct ctt   2016
203 Gly Thr Arg Leu Glu Pro Pro Ala Pro Gln Ile Ser Ala Leu Ala Leu
204           660             665             670
206 cat cat ttc acg gac tta tcc aat aac aac gac ttt tat atc cta taa   2064
207 His His Phe Thr Asp Leu Ser Asn Asn Asn Asp Phe Tyr Ile Leu
208           675             680             685
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 687
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapiens
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (598)..(598)
219 <223> OTHER INFORMATION: The 'Xaa' at location 598 stands for Thr or Pro.
221 <400> SEQUENCE: 2
223 Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
224 1               5               10              15
227 Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
228           20              25              30
231 Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
232           35              40              45
235 Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
236       50              55              60
239 Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
240 65              70              75              80
243 Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
244           85              90              95
247 Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
248           100             105             110
251 Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
252       115             120             125
255 Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
256       130             135             140
259 Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
260 145             150             155             160
263 Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
264           165             170             175
267 Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
268           180             185             190
271 Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
272       195             200             205
275 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
276       210             215             220
279 Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
```

```
                    Input Set : A:\3151-A SeqListce 102601.txt
                    Output Set: N:\CRF3\02222002\J061727.raw

        280 225                   230              235                  240
        283 Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
        284             245             250             255
        287 Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
        288             260             265             270
        291 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
        292         275             280             285
        295 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
        296     290             295             300
        299 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
        300 305             310             315                  320
        303 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
        304             325             330             335
        307 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
        308             340             345             350
        311 Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
        312         355             360             365
        315 Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
        316     370             375             380
        319 Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
        320 385             390             395                  400
        323 Asp Gly Lys Glu Tyr Asp Ile Tyr Val Ser Tyr Ala Arg Asn Ala Glu
        324             405             410             415
        327 Glu Glu Glu Phe Val Leu Leu Thr Leu Arg Gly Val Leu Glu Asn Glu
        328             420             425             430
        331 Phe Gly Tyr Lys Leu Cys Ile Phe Asp Arg Asp Ser Leu Pro Gly Gly
        332         435             440             445
        335 Asn Thr Val Glu Ala Val Phe Asp Phe Ile Gln Arg Ser Arg Arg Met
        336     450             455             460
        339 Ile Val Val Leu Ser Pro Asp Tyr Val Thr Glu Lys Ser Ile Ser Met
        340 465             470             475                  480
        343 Leu Glu Phe Lys Leu Gly Val Met Cys Gln Asn Ser Ile Ala Thr Lys
        344             485             490             495
        347 Leu Ile Val Val Glu Tyr Arg Pro Leu Glu His Pro His Pro Gly Ile
        348             500             505             510
        351 Leu Gln Leu Lys Glu Ser Val Ser Phe Val Ser Trp Lys Gly Glu Lys
        352         515             520             525
        355 Ser Lys His Ser Gly Ser Lys Phe Trp Lys Ala Leu Arg Leu Ala Leu
        356     530             535             540
        359 Pro Leu Arg Ser Leu Ser Ala Ser Ser Gly Trp Asn Glu Ser Cys Ser
        360 545             550             555                  560
        363 Ser Gln Ser Asp Ile Ser Leu Asp His Val Gln Arg Arg Arg Ser Arg
        364             565             570             575
        367 Leu Lys Glu Pro Pro Glu Leu Gln Ser Ser Glu Arg Ala Ala Gly Ser
        368             580             585             590
W--> 371 Pro Pro Ala Pro Gly Xaa Met Ser Lys His Arg Gly Lys Ser Ser Ala
        372         595             600             605
        375 Thr Cys Arg Cys Cys Val Thr Tyr Cys Glu Gly Glu Asn His Leu Arg
        376     610             615             620
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VERIFICATION SUMMARY   DATE: 02/22/2002
PATENT APPLICATION: US/10/061,727   TIME: 16:08:43

Input Set : **A:\3151-A SeqListce 102601.txt**
Output Set: **N:\CRF3\02222002\J061727.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2